Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:51:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716641.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR9716641 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716641.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:51:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716641.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	855,466
Mapped reads	778,132 / 90.96%
Unmapped reads	77,334 / 9.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,498 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	20,887 / 2.44%
Duplication rate	1.87%
Clipped reads	779,409 / 91.11%

2.2. ACGT Content

Number/percentage of A's	10,724,516 / 24.15%
Number/percentage of C's	8,123,067 / 18.29%
Number/percentage of T's	14,552,383 / 32.76%
Number/percentage of G's	11,013,588 / 24.8%
Number/percentage of N's	914 / 0%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1658

2.4. Mapping Quality

Mean Mapping Quality	43.91

2.5. Mismatches and indels

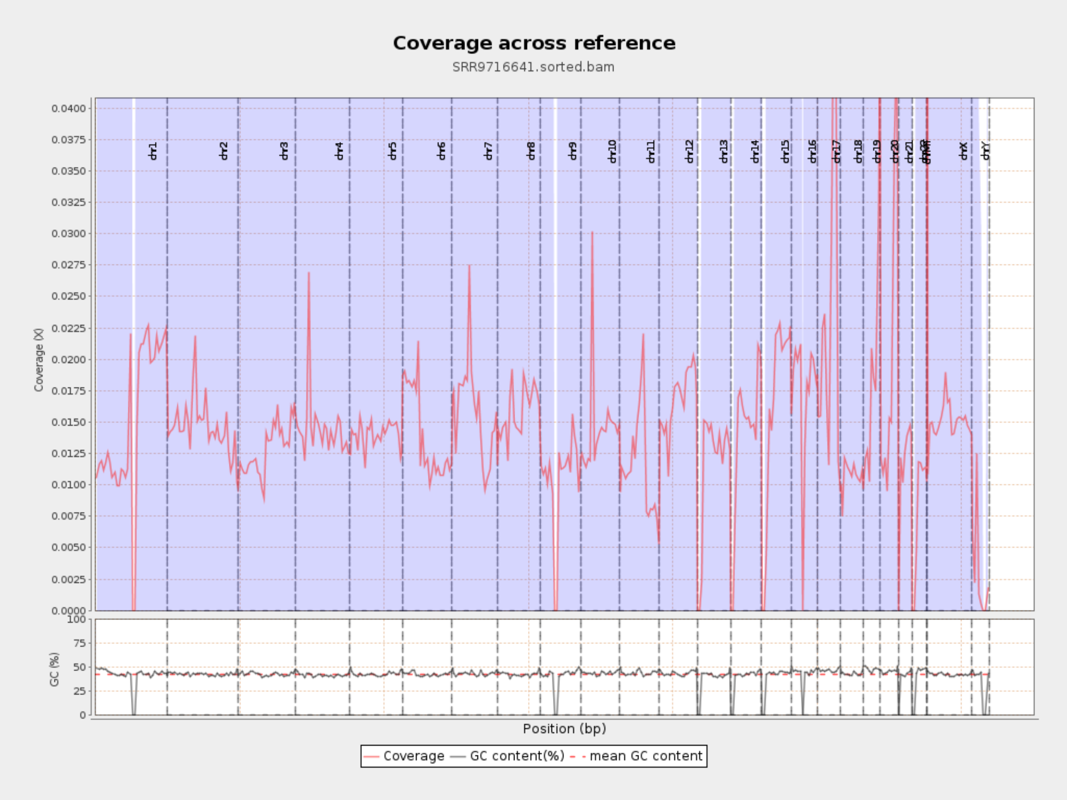
General error rate	0.53%
Mismatches	229,950
Insertions	2,856
Mapped reads with at least one insertion	0.37%
Deletions	8,767
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.84%

2.6. Chromosome stats

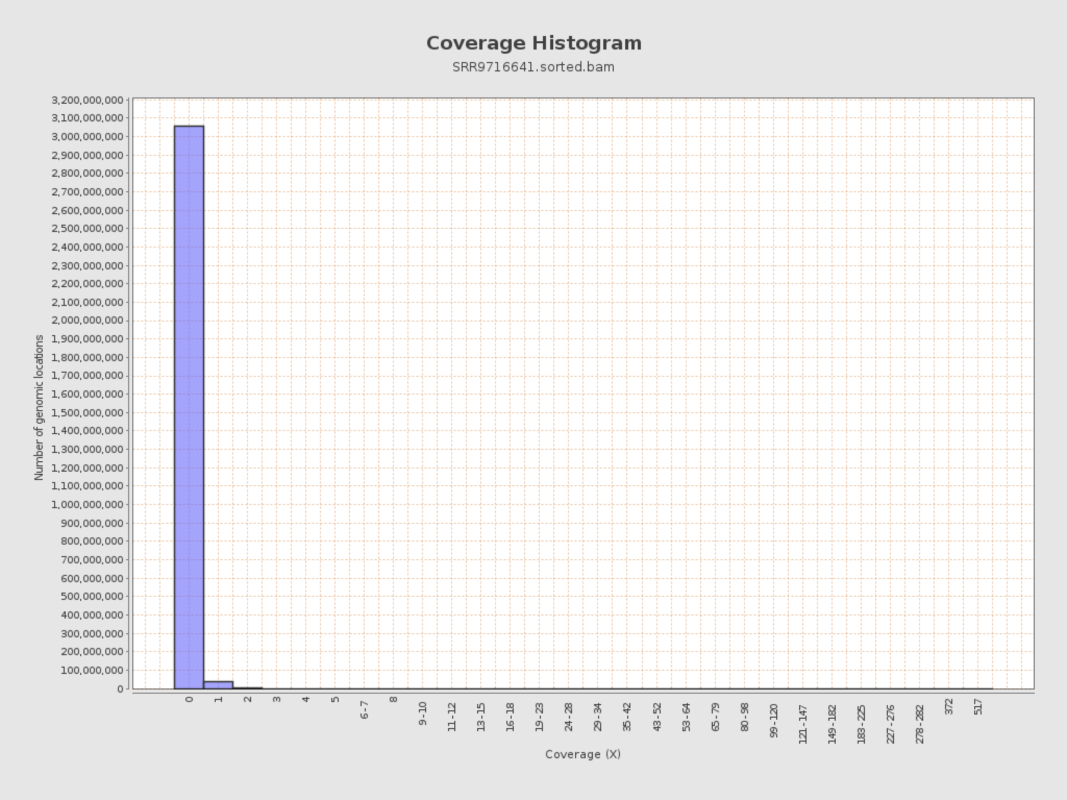
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3746932	0.015	0.2325
chr2	243199373	3563600	0.0147	0.2406
chr3	198022430	2532041	0.0128	0.1196
chr4	191154276	2784641	0.0146	0.1419
chr5	180915260	2544165	0.0141	0.124
chr6	171115067	2400307	0.014	0.1385
chr7	159138663	2530481	0.0159	0.2089

chr8	146364022	2339926	0.016	0.2057
chr9	141213431	1470598	0.0104	0.1207
chr10	135534747	1977318	0.0146	0.1744
chr11	135006516	1580781	0.0117	0.1303
chr12	133851895	2244603	0.0168	0.1369
chr13	115169878	1320350	0.0115	0.1131
chr14	107349540	1484760	0.0138	0.1238
chr15	102531392	1647591	0.0161	0.1328
chr16	90354753	1541353	0.0171	0.1402
chr17	81195210	1948601	0.024	0.1655
chr18	78077248	834928	0.0107	0.1721
chr19	59128983	1107500	0.0187	0.2061
chr20	63025520	1301267	0.0206	0.1534
chr21	48129895	560725	0.0117	0.1352
chr22	51304566	414754	0.0081	0.0942
chrMT	16571	32364	1.9531	1.7415
chrX	155270560	2344998	0.0151	0.1358
chrY	59373566	174158	0.0029	0.1337

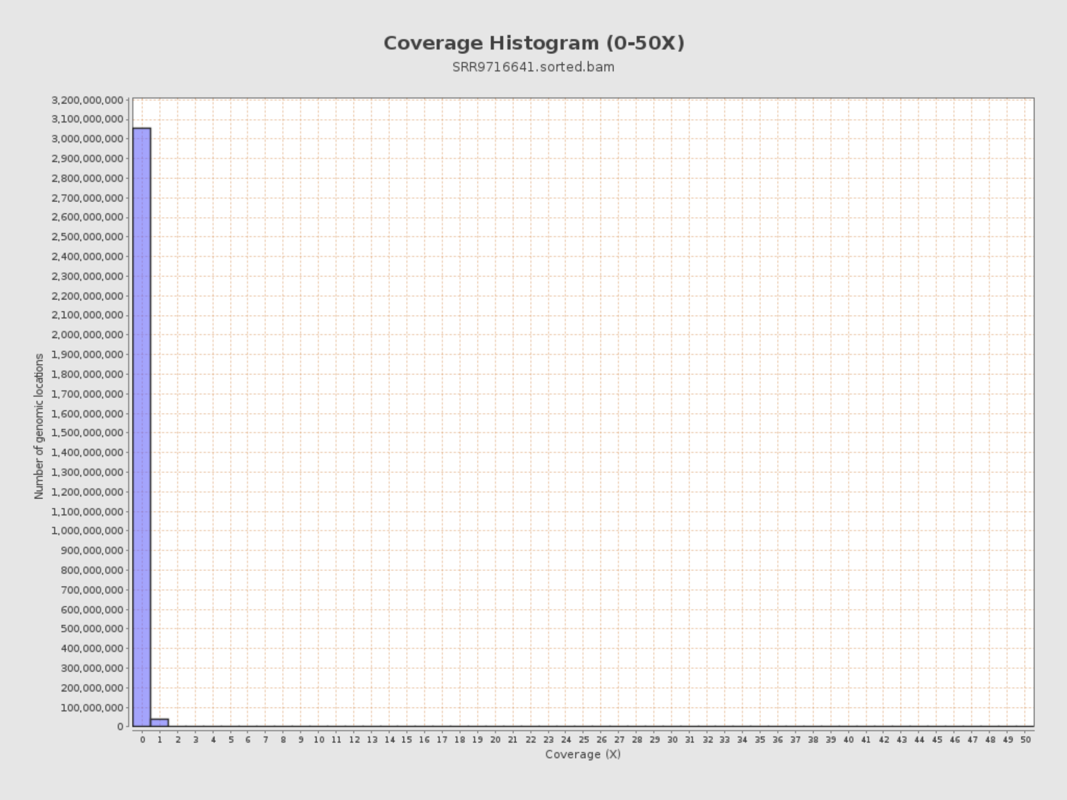
3. Results : Coverage across reference



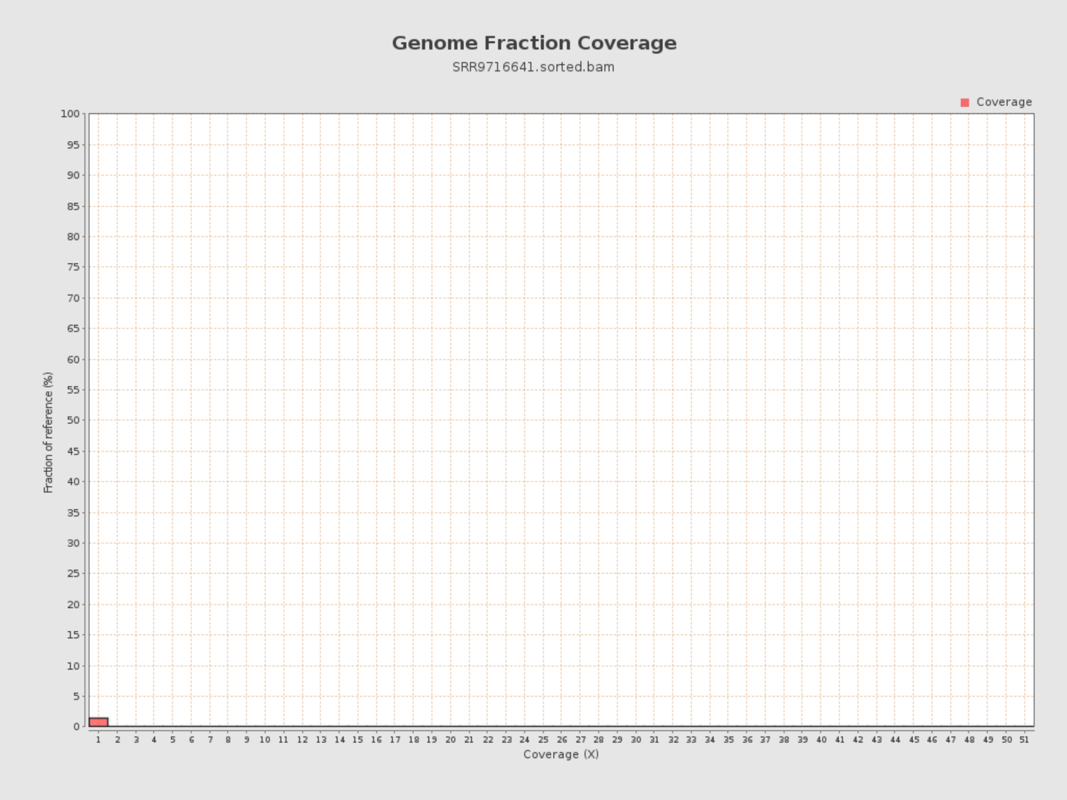
4. Results : Coverage Histogram



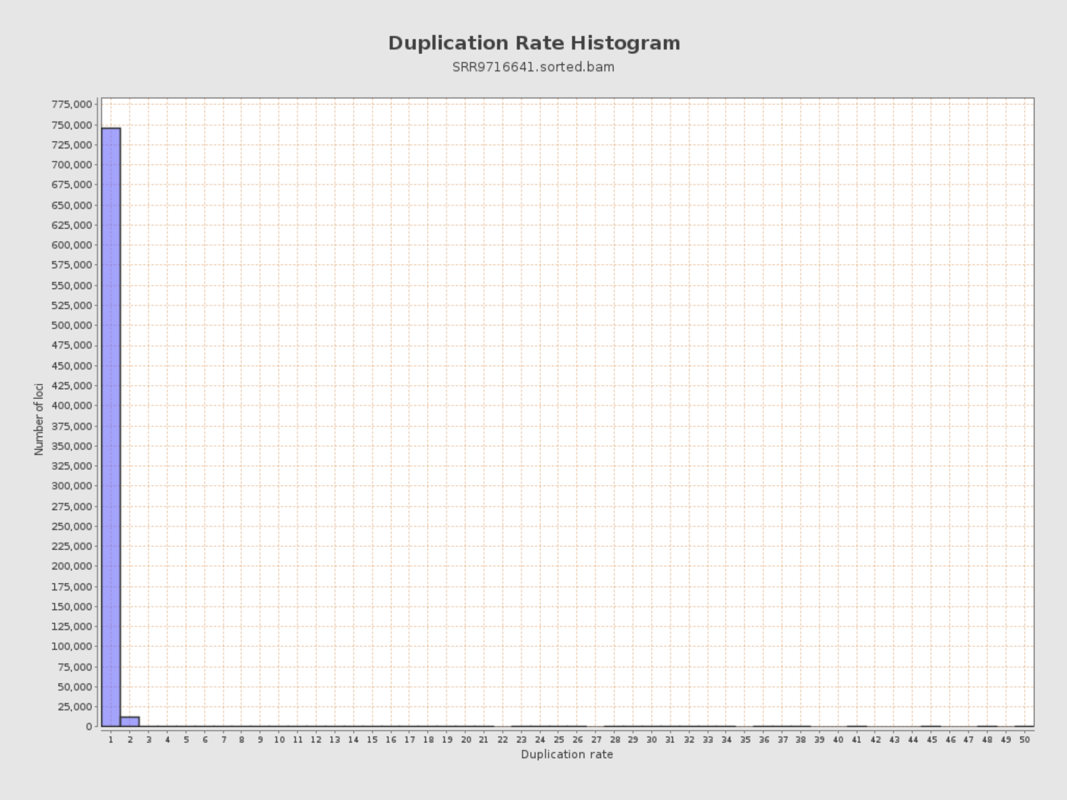
5. Results : Coverage Histogram (0-50X)



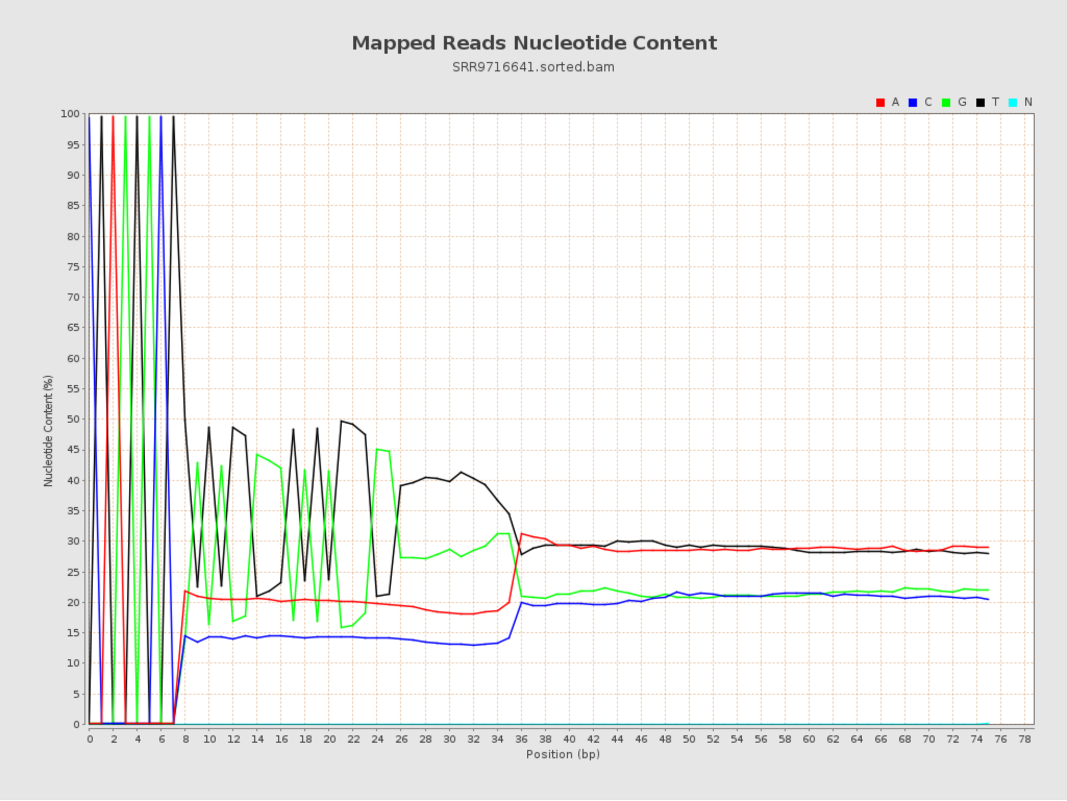
6. Results : Genome Fraction Coverage



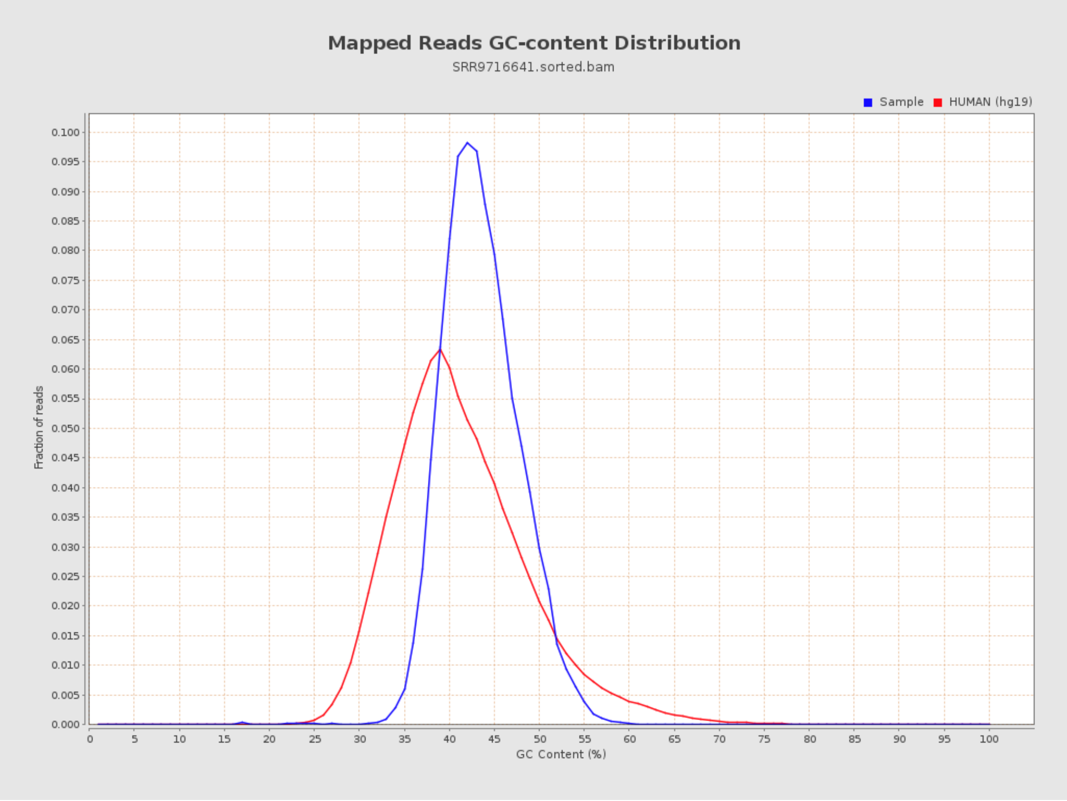
7. Results : Duplication Rate Histogram



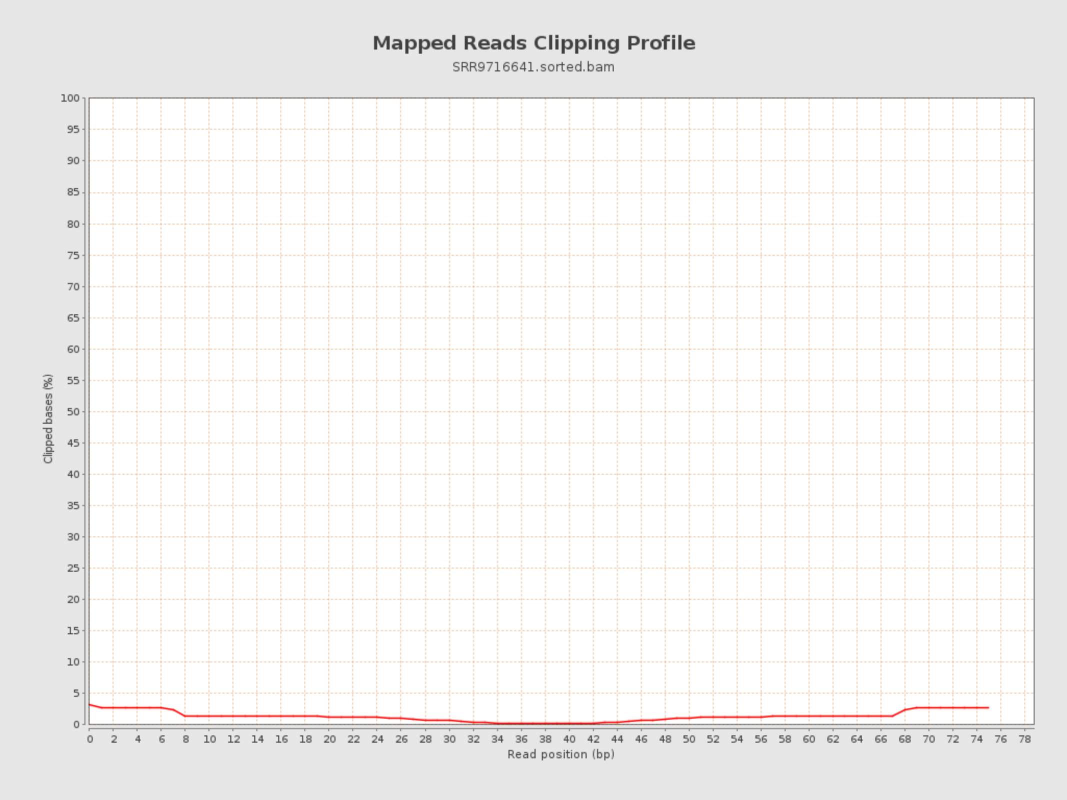
8. Results : Mapped Reads Nucleotide Content



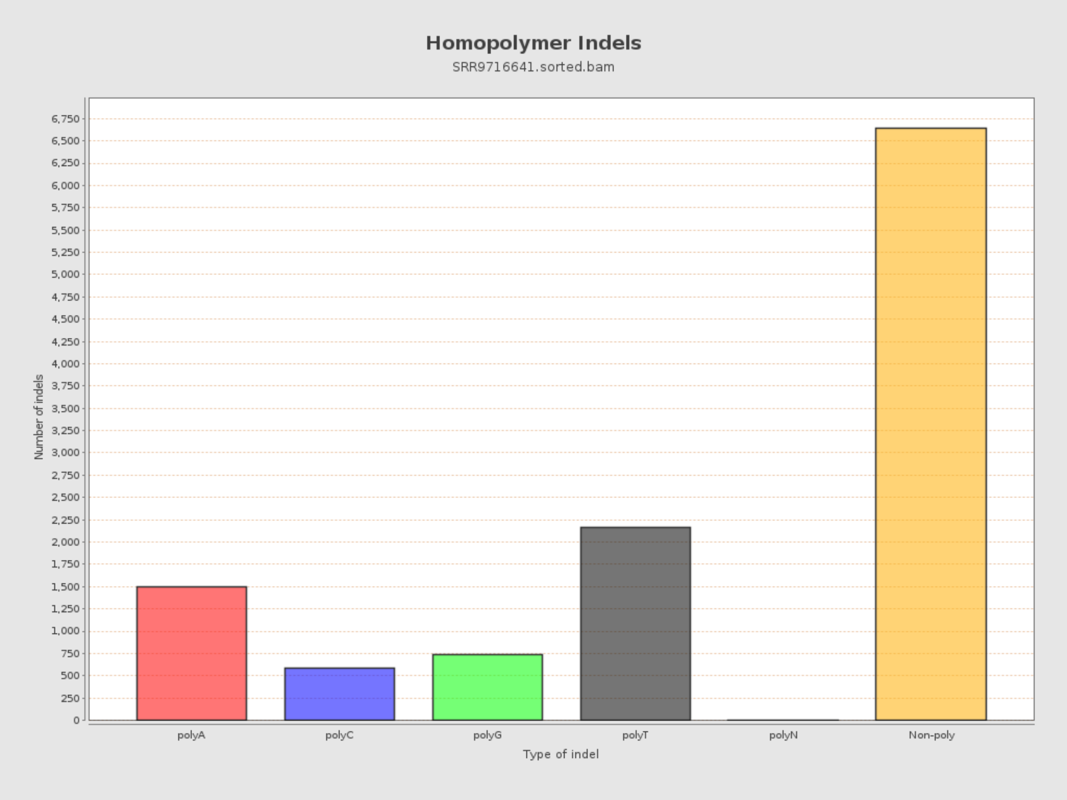
9. Results : Mapped Reads GC-content Distribution



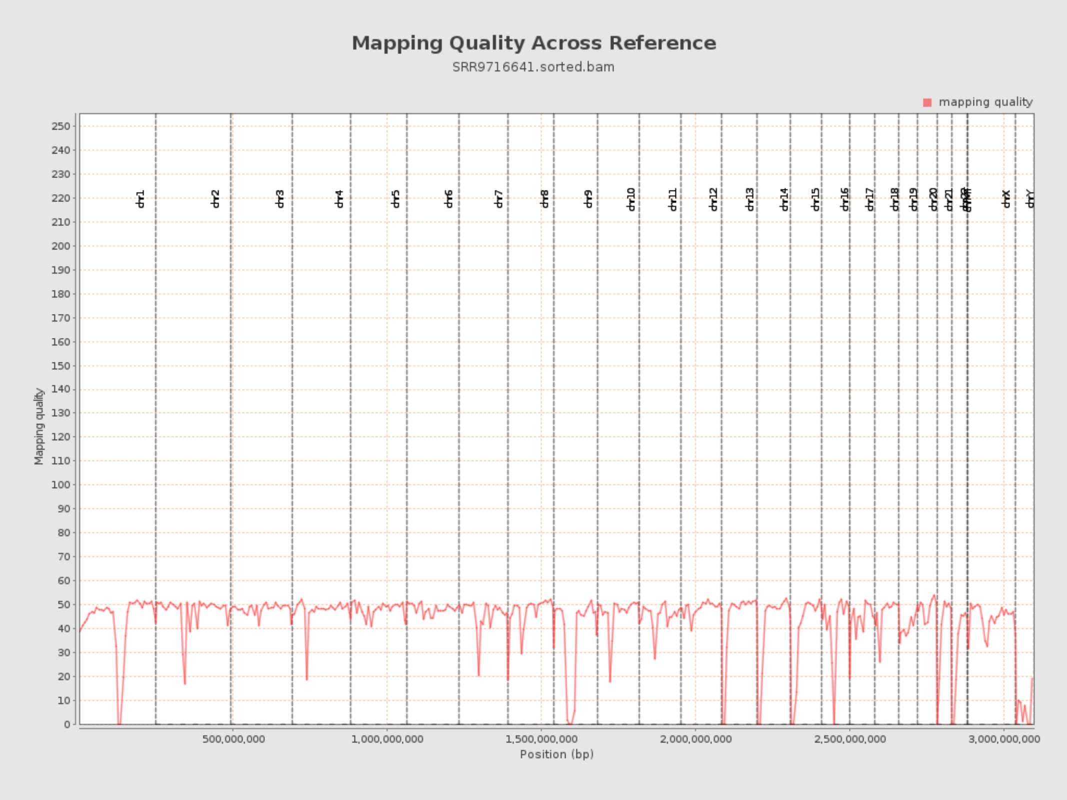
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram